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43

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SEQUENCE LISTING

<110> Kovesdi, Imre
Kessler, Paul

<120> VEGF FUSION PROTEINS

<130> 205654

<140> US 09/832,355

<141> 2001-04-10

<160> 126

<170> PatentIn version 3.0

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Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys
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Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu
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Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile
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Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe
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Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly
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20 25 30

Tyr Asn Arg Ile Gln His Gly Gln Cys Ala Tyr Thr Phe Ile Leu Pro
 35 40 45

Glu His Asp Gly Asn Cys Arg Glu Ser Thr Thr Asp Gln Tyr Asn Thr
 50 .55 60

Asn Ala Leu Gln Arg Asp Ala Pro His Val Glu Pro Asp Phe Ser Ser
65 70 75 80

Gln Lys Leu Gln His Leu Glu His Val Met Glu Asn Tyr Thr Gln Trp
85 90 95

Leu Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met
100 105 110

Ala Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu
115 120 125

Glu Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys
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Leu Leu Glu His Lys Ile Leu Glu Met Glu Gly Lys His Lys Glu Glu
195 200 205

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210 215 220

Arg Gln Thr Tyr Ile Ile Gln Glu Leu Glu Lys Gin Leu Asn Arg Ala
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 Thr Val His Asn Leu Val Asn Leu Cys Thr Lys Glu Gly Val Leu Leu
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 Asn Asn Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn
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 Gly Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp
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 Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn
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 Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser
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 Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn
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 Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp
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 Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala
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Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg
 85 90 95

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu
 100 105 110

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asn
 115 120 125

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp
 130 135 140

Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln
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 35 40 45

Gln Lys Leu Glu Asn Tyr Ile Val Glu Asn Met Lys Ser Glu Met Ala
 50 55 60

Gln Ile Gln Gln Asn Ala Val Gln Asn His Thr Ala Thr Met Leu Glu
 65 70 75 80

Ile Gly Thr Ser Leu Leu Ser Gln Thr Ala Glu Gln Thr Arg Lys Leu
 85 90 95

Thr Asp Val Glu Thr Gln Val Leu Asn Gln Thr Ser Arg Leu Glu Ile
 100 105 110

Gln Leu Leu Glu Asn Ser Leu Ser Thr Tyr Lys Leu Glu Lys Gln Leu
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Leu Gln Gln Thr Asn Glu Ile Leu Lys Ile His Glu Lys Asn Ser Leu
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Thr Asn Asn Ser Val Leu Gln Lys Gln Gln Leu Glu Leu Met Asp Thr			
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Val Asn Cys Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg			
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Ala Gly Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys			
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Val His Ser Ile Met Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu			
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Gly Gly Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala
 115 120 125

Gly Gln Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro
 130 135 140

Phe Ser Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys
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 35 40 45

Ile Ile Gln Arg Arg Glu Asp Gly Ser Val Asp Phe Gln Arg Thr Trp
 50 55 60

Lys Glu Tyr Lys Val Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu
 65 70 75 80

Gly Asn Glu Phe Val Ser Gln Leu Thr Asn Gln Gln Arg Tyr Val Leu
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Lys Ile His Leu Lys Asp Trp Glu Gly Asn Glu Ala Tyr Ser Leu Tyr
 100 105 110

Glu His Phe Tyr Leu Ser Ser Glu Glu Leu Asn Tyr Arg Ile His Leu
 115 120 125

Lys Gly Leu Thr Gly Thr Ala Gly Lys Ile Ser Ser Ile Ser Gln Pro
 130 135 140

Gly Asn Asp Phe Ser Thr Lys Asp Gly Asp Asn Asp Lys Cys Ile Cys
 145 150 155 160

Lys Cys Ser Gln Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly
 165 170 175

Pro Ser Asn Leu Asn Gly Met Tyr Tyr Pro Gln Arg Gln Asn Thr Asn
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 Lys Phe Asn Gly Ile Lys Trp Tyr Tyr Trp Lys Gly Ser Gly Tyr Ser
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 Arg Ser Trp Ser Ser Tyr Arg Ala Gly Phe Gly Asn Gln Glu Ser Glu
 65 70 75 80
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 85 90 95
 Trp Glu Leu Arg Val Glu Leu Glu Asp Phe Asn Gly Asn Arg Thr Phe
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 Ala His Tyr Ala Thr Phe Arg Leu Leu Gly Glu Val Asp His Tyr Gln
 115 120 125
 Leu Ala Leu Gly Lys Phe Ser Glu Gly Thr Ala Gly Asp Ser Leu Ser
 130 135 140
 Leu His Ser Gly Arg Pro Phe Thr Thr Tyr Asp Ala Asp His Asp Ser
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 165 170 175
 Ser Cys Tyr Arg Ser Asn Leu Asn Gly Arg Tyr Ala Val Ser Glu Ala
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Cys	Asp	Met	Glu	Thr	Ser	Gly	Gly	Trp	Thr	Ile	Ile	Gln	Arg	Arg
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Lys	Ser	Gly	Leu	Val	Ser	Phe	Tyr	Arg	Asp	Trp	Lys	Gln	Tyr	Lys	Gln
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Gly	Phe	Gly	Ser	Ile	Arg	Gly	Asp	Phe	Trp	Leu	Gly	Asn	Glu	His	Ile
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Trp	Glu	Gly	Asn	Leu	Arg	Tyr	Ala	Glu	Tyr	Ser	His	Phe	Val	Leu	Gly
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Asn	Glu	Leu	Asn	Ser	Tyr	Arg	Leu	Phe	Leu	Gly	Asn	Tyr	Thr	Gly	Asn
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Val	Gly	Asn	Asp	Ala	Leu	Gln	Tyr	His	Asn	Asn	Thr	Ala	Phe	Ser	Thr
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Lys	Asp	Lys	Asp	Asn	Asp	Asn	Cys	Leu	Asp	Lys	Cys	Ala	Gln	Leu	Arg
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Lys	Gly	Gly	Tyr	Trp	Tyr	Asn	Cys	Cys	Thr	Asp	Ser	Asn	Leu	Asn	Gly
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Val	Tyr	Tyr	Arg	Leu	Gly	Glu	His	Asn	Lys	His	Leu	Asp	Gly	Ile	Thr
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Trp	Tyr	Gly	Trp	His	Gly	Ser	Thr	Tyr	Ser	Leu	Lys	Arg	Val	Glu	Met
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Lys	Pro	Val	Gly	Pro	Trp	Gln	Asp	Cys	Ala	Glu	Ala	Arg	Gln	Ala	Gly
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His	Glu	Gln	Ser	Gly	Val	Tyr	Glu	Leu	Arg	Val	Gly	Arg	His	Val	Val
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20

25

30

Ser Val Trp Cys Glu Gln Gln Leu Glu Gly Gly Trp Thr Val Ile
 35 40 45

Gln Arg Arg Gln Asp Gly Ser Val Asn Phe Phe Thr Thr Trp Gln His
 50 55 60

Tyr Lys Ala Gly Phe Gly Arg Pro Asp Gly Glu Tyr Trp Leu Gly Leu
 65 70 75 80

Glu Pro Val Tyr Gln Leu Thr Ser Arg Gly Asp His Glu Leu Leu Val
 85 90 95

Leu Leu Glu Asp Trp Gly Gly Arg Gly Ala Arg Ala His Tyr Asp Gly
 100 105 110

Phe Ser Leu Glu Pro Glu Ser Asp His Tyr Arg Leu Arg Leu Gly Gln
 115 120 125

Tyr His Gly Asp Ala Gly Asp Ser Leu Ser Trp His Asn Asp Lys Pro
 130 135 140

Phe Ser Thr Val Asp Arg Asp Arg Asp Ser Tyr Ser Gly Asn Cys Ala
 145 150 155 160

Leu Tyr Gln Arg Gly Gly Trp Trp Tyr His Ala Cys Ala His Ser Asn
 165 170 175

Leu Asn Gly Val Trp His His Gly Gly His Tyr Arg Ser Arg Tyr Gln
 180 185 190

Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ala Tyr Ser Leu Arg
 195 200 205

Lys Ala Ala Met Leu Ile Arg Pro Leu Lys Leu
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<210> 25

<211> 215

<212> PRT

<213> Homo sapiens

<400> 25

Leu Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser
 1 5 10 15

Gly Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn
 20 25 30

Cys Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His
 35 40 45

Asp Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly
 50 55 60

Phe Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His
 65 70 75 80

Ser Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp
85 90 95

Trp Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly
100 105 110

Glu Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln
115 120 125

Leu Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser
130 135 140

Thr Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys
145 150 155 · 160

Ser Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu
165 170 175

Asn Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys
 180 185 190

Lys Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln
 195 200 205

Ala Thr Thr Met Leu Ile Gln
210 215

<210> 26

<211> 222

<212> PRT

<213> Artificial sequence

<220>

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<222> () . . ()

<223> Source not known

<400> 26

Pro Arg Asp Cys Gln Glu Leu Phe Gln Val Gly Glu Arg Gln Ser Gly
1 5 10 15

Leu Phe Glu Ile Gln Pro Gln Gly Ser Pro Pro Phe Leu Val Asn Cys
20 25 30

Lys Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg His Asp
35 40 45

Gly Ser Val Asp Phe Asn Arg Pro Trp Glu Ala Tyr Lys Ala Gly Phe
50 55 60

Gly Asp Pro His Gly Glu Phe Trp Leu Gly Leu Glu Lys Val His Ser
 65 70 75 80

Ile Thr Gly Asp Arg Asn Ser Arg Leu Ala Val Gln Leu Arg Asp Trp
85 90 95

Asp Gly Asn Ala Glu Leu Leu Gln Phe Ser Val His Leu Gly Gly Glu

100

105

110

Asp Thr Ala Tyr Ser Leu Gln Leu Thr Ala Pro Val Ala Gly Gln Leu
 115 120 125

Gly Ala Thr Thr Val Pro Pro Ser Gly Leu Ser Val Pro Phe Ser Thr
 130 135 140

Trp Asp Gln Asp His Asp Leu Arg Arg Asp Lys Asn Cys Ala Lys Ser
 145 150 155 160

Leu Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn
 165 170 175

Gly Gln Tyr Phe Arg Ser Ile Pro Gln Gln Arg Gln Lys Leu Lys Lys
 180 185 190

Gly Ile Phe Trp Lys Thr Trp Arg Gly Arg Tyr Tyr Pro Leu Gln Ala
 195 200 205

Thr Thr Met Leu Ile Gln Pro Met Ala Ala Glu Ala Ala Ser
 210 215 220

<210> 27

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()...()

<223> Source not known

<400> 27

His Asp Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu
 1 5 10 15

His Thr Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe
 20 25 30

His Val Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln
 35 40 45

His Arg Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr
 50 55 60

Lys Tyr Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu
 65 70 75 80

Lys Ile Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu
 85 90 95

Leu Glu Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr
 100 105 110

Leu Gly Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr
 115 120 125

Gly Asn Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser
130 135 140

Thr Trp Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr
145 150 155 160

Ser Gly Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn
165 170 175

Gly Lys Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg
180 185 190

Gly Leu Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser
195 200 205

Thr Lys Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
210 215 220

<210> 28
<211> 214
<212> PRT
<213> Mus musculus

<400> 28

Arg Asp Cys Gln Glu Leu Phe Gln Glu Gly Glu Arg His Ser Gly Leu
1 5 10 15

Phe Gln Ile Gln Pro Leu Gly Ser Pro Pro Phe Leu Val Asn Cys Glu
20 25 30

Met Thr Ser Asp Gly Gly Trp Thr Val Ile Gln Arg Arg Leu Asn Gly
35 40 45

Ser Val Asp Phe Asn Gln Ser Trp Glu Ala Tyr Lys Asp Gly Phe Gly
50 55 60

Asp Pro Gln Gly Glu Phe Trp Leu Gly Leu Glu Lys Met His Ser Ile
65 70 75 80

Thr Gly Asn Arg Gly Ser Gln Leu Ala Val Gln Leu Gln Asp Trp Asp
85 90 95

Gly Asn Ala Lys Leu Leu Gln Phe Pro Ile His Leu Gly Gly Glu Asp
100 105 110

Thr Ala Tyr Ser Leu Gln Leu Thr Glu Pro Thr Ala Asn Glu Leu Gly
115 120 125

Ala Thr Asn Val Ser Pro Asn Gly Leu Ser Leu Pro Phe Ser Thr Trp
130 135 140

Asp Gln Asp His Asp Leu Arg Gly Asp Leu Asn Cys Ala Lys Ser Leu
145 150 155 160

Ser Gly Gly Trp Trp Phe Gly Thr Cys Ser His Ser Asn Leu Asn Gly
165 170 175

Gln Tyr Phe His Ser Ile Pro Arg Gln Arg Gln Glu Arg Lys Lys Gly

180

185

190

Ile Phe Trp Lys Thr Trp Lys Gly Arg Tyr Tyr Pro Leu Gln Ala Thr
 195 200 205

Thr Leu Leu Ile Gln Pro
 210

<210> 29
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 29

Phe Gln Asp Cys Ala Glu Ile Lys Arg Ser Gly Val Asn Thr Ser Gly
 1 5 10 15

Val Tyr Thr Ile Tyr Glu Thr Asn Met Thr Lys Pro Leu Lys Val Phe
 20 25 30

Cys Asp Met Glu Thr Asp Gly Gly Trp Thr Leu Ile Gln His Arg
 35 40 45

Glu Asp Gly Ser Val Asn Phe Gln Arg Thr Trp Glu Glu Tyr Lys Glu
 50 55 60

Gly Phe Gly Asn Val Ala Arg Glu His Trp Leu Gly Asn Glu Ala Val
 65 70 75 80

His Arg Leu Thr Ser Arg Thr Ala Tyr Leu Leu Arg Val Glu Leu His
 85 90 95

Asp Trp Glu Gly Arg Gln Thr Ser Ile Gln Tyr Glu Asn Phe Gln Leu
 100 105 110

Gly Ser Glu Arg Gln Arg Tyr Ser Leu Ser Val Asn Asp Ser Ser Ser
 115 120 125

Ser Ala Gly Arg Lys Asn Ser Leu Ala Pro Gln Gly Thr Lys Phe Ser
 130 135 140

Thr Lys Asp Met Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Gln Met
 145 150 155 160

Leu Ser Gly Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn
 165 170 175

Gly Ile Tyr Tyr Ser Val His Gln His Leu His Lys Ile Asn Gly Ile
 180 185 190

Arg Trp His Tyr Phe Arg Gly Pro Ser Tyr Ser Leu His Gly Thr Arg
 195 200 205

Met Met Leu Arg Pro Met Gly Ala
 210 215

<210> 30
 <211> 216

<212> PRT

<213> Homo sapiens

<400> 30

Phe Gln Asp Cys Ala Glu Ile Gln Arg Ser Gly Ala Ser Ala Ser Gly
1 5 10 15

Val Tyr Thr Ile Gln Val Ser Asn Ala Thr Lys Pro Arg Lys Val Phe
20 25 30

Cys Asp Leu Gln Ser Ser Gly Gly Arg Trp Thr Leu Ile Gln Arg Arg
35 40 45

Glu Asn Gly Thr Val Asn Phe Gln Arg Asn Trp Lys Asp Tyr Lys Gln
50 55 60

Gly Phe Gly Asp Pro Ala Gly Glu His Trp Leu Gly Asn Glu Val Val
65 70 75 80

His Gln Leu Thr Arg Arg Ala Ala Tyr Ser Leu Arg Val Glu Leu Gln
85 90 95

Asp Trp Glu Gly His Glu Ala Tyr Ala Gln Tyr Glu His Phe His Leu
100 105 110

Gly Ser Glu Asn Gln Leu Tyr Arg Leu Ser Val Val Gly Tyr Ser Gly
115 120 125

Ser Ala Gly Arg Gln Ser Ser Leu Val Leu Gln Asn Thr Ser Phe Ser
130 135 140

Thr Leu Asp Ser Asp Asn Asp His Cys Leu Cys Lys Cys Ala Gln Val
145 150 155 160

Met Ser Gly Trp Trp Phe Asp Ala Cys Gly Leu Ser Asn Leu Asn
165 170 175

Gly Val Tyr Tyr His Ala Pro Asp Asn Lys Tyr Lys Met Asp Gly Ile
180 185 190

Arg Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ala Ser Arg
195 200 205

Met Met Ile Arg Pro Leu Asp Ile
210 215

<210> 31

<211> 224

<212> PRT

<213> Homo sapiens

<400> 31

Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly
1 5 10 15

His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg
20 25 30

Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr
 35 40 45

Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp
 50 55 60

Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu
 65 70 75 80

Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu
 85 90 95

Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr
 100 105 110

Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu
 115 120 125

Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly
 130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn
 145 150 155 160

Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His
 165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg
 180 185 190

Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser
 195 200 205

Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
 210 215 220

<210> 32

<211> 220

<212> PRT

<213> Homo sapiens

<400> 32

Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys Glu Ala Gly
 1 5 10 15

His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn Ser Asn Gly
 20 25 30

Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly Gly Trp Thr
 35 40 45

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp
 50 55 60

Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu
 65 70 75 80

Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu
85 90 95

Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr
100 105 110

Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu
115 120 125

Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly
130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn
145 150 155 160

Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His
165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys
180 185 190

His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Ser Tyr Ser
195 200 205

Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
210 215 220

<210> 33

<211> 136

<212> PRT

<213> Homo sapiens

<400> 33

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
1 5 10 15

Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
20 25 30

Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
35 40 45

Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
50 55 60

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
65 70 75 80

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
85 90 95

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
100 105 110

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly
115 120 125

Lys Lys Gln Glu Lys Met Leu Asp

130 135

<210> 34
<211> 121
<212> PRT
<213> Homo sapiens

<400> 34

Lys Lys Lys Asp Lys Val Lys Lys Gly Gly Pro Gly Ser Glu Cys Ala
1 5 10 15

Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser Ser Lys Asp Cys Gly Val
20 25 30

Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln Thr Gln Arg Ile Arg Cys
35 40 45

Arg Val Pro Cys Asn Trp Lys Lys Glu Phe Gly Ala Asp Cys Lys Tyr
50 55 60

Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Thr Gly Thr Lys Val
65 70 75 80

Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu
85 90 95

Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala
100 105 110

Lys Ala Lys Lys Gly Lys Gly Lys Asp
115 120

<210> 35
<211> 43
<212> PRT
<213> Homo sapiens

<400> 35

Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn Thr Ala
1 5 10 15

Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn Ala Glu
20 25 30

Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys
35 40

<210> 36
<211> 54
<212> PRT
<213> Homo sapiens

<400> 36

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
 35 40 45

Thr Lys Pro Lys Pro Gln
 50

<210> 37

<211> 72

<212> PRT

<213> Homo sapiens

<400> 37

Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
 1 5 10 15

Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
 20 25 30

Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
 35 40 45

Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly
 50 55 60

Lys Lys Gln Glu Lys Met Leu Asp
 65 70

<210> 38

<211> 80

<212> PRT

<213> Homo sapiens

<400> 38

Cys Gly Glu Trp Thr Trp Gly Pro Cys Ile Pro Asn Ser Lys Asp Cys
 1 5 10 15

Gly Leu Gly Thr Arg Glu Gly Thr Cys Lys Gln Glu Thr Arg Lys Leu
 20 25 30

Lys Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly Ala Asp Cys
 35 40 45

Lys Tyr Lys Phe Glu Ser Trp Gly Glu Cys Asp Ala Asn Thr Gly Leu
 50 55 60

Lys Thr Arg Ser Gly Thr Leu Lys Lys Ala Leu Tyr Asn Ala Asp Cys
 65 70 75 80

<210> 39

<211> 21

<212> PRT

<213> Homo sapiens

<400> 39

Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
1 5 10 15

Glu Trp Gln Trp Ser
20

<210> 40
<211> 16
<212> PRT
<213> Homo sapiens

<400> 40

Ser Lys Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp
1 5 10 15

<210> 41
<211> 61
<212> PRT
<213> Homo sapiens

<400> 41

Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr
1 5 10 15

Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala
20 25 30

Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro Lys Thr
35 40 45

Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
50 55 60

<210> 42
<211> 42
<212> PRT
<213> Homo sapiens

<400> 42

Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly Gly Thr Gly Thr
1 5 10 15

Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr Asn Ala Gln Cys
20 25 30

Gln Glu Thr Ile Arg Val Thr Lys Pro Cys
35 40

<210> 43
<211> 32
<212> PRT
<213> Homo sapiens

<400> 43

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
 1 5 10 15

Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
 20 25 30

<210> 44

<211> 20

<212> PRT

<213> Homo sapiens

<400> 44

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala
 20

<210> 45

<211> 139

<212> PRT

<213> Homo sapiens

<400> 45

Phe Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys
 1 5 10 15

Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp
 20 25 30

Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala
 35 40 45

Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr
 50 55 60

Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn
 65 70 75 80

Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr
 85 90 95

Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys
 100 105 110

Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys
 115 120 125

Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser
 130 135

<210> 46

<211> 15

<212> PRT

<213> Homo sapiens

<400> 46

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys
1 5 10 15

<210> 47
<211> 8
<212> PRT
<213> Homo sapiens

<400> 47

Lys Lys Asn Gly Ser Cys Lys Arg
1 5

<210> 48
<211> 13
<212> PRT
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<220>
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<222> ()..()
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<220>
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<222> (5)..(5)
<223> "Xaa" may be between 5 and 7 of any amino acids

<220>
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<222> (7)..(9)
<223> "Xaa" may be any amino acid

<400> 48

Arg Leu Tyr Cys Xaa Leu Xaa Xaa Xaa Pro Asp Gly Arg
1 5 10

<210> 49
<211> 4
<212> PRT
<213> Homo sapiens

<400> 49

Ile Ser Ser Lys
1

<210> 50
<211> 5
<212> PRT
<213> Homo sapiens

<400> 50

Lys Lys Pro Lys Leu
1 5

<210> 51
<211> 535
<212> PRT
<213> Homo sapiens

<400> 51

Met Leu Gly Pro Cys Met Leu Leu Leu Leu Leu Leu Gly Leu Arg
1 5 10 15

Leu Gln Leu Ser Leu Gly Ile Ile Pro Val Glu Glu Asn Pro Asp
20 25 30

Phe Trp Asn Arg Glu Ala Ala Glu Ala Leu Gly Ala Ala Lys Lys Leu
35 40 45

Gln Pro Ala Gln Thr Ala Ala Lys Asn Leu Ile Ile Phe Leu Gly Asp
50 55 60

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln
65 70 75 80

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe
85 90 95

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro
100 105 110

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn
115 120 125

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn
130 135 140

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys
145 150 155 160

Ala Gly Lys Ser Val Gly Val Val Thr Thr Arg Val Gln His Ala
165 170 175

Ser Pro Ala Gly Thr Tyr Ala His Thr Val Asn Arg Asn Trp Tyr Ser
180 185 190

Asp Ala Asp Val Pro Ala Ser Ala Arg Gln Glu Gly Cys Gln Asp Ile
195 200 205

Ala Thr Gln Leu Ile Ser Asn Met Asp Ile Asp Val Ile Leu Gly Gly
210 215 220

Gly Arg Lys Tyr Met Phe Arg Met Gly Thr Pro Asp Pro Glu Tyr Pro
225 230 235 240

Asp Asp Tyr Ser Gln Gly Gly Thr Arg Leu Asp Gly Lys Asn Leu Val
245 250 255

Gln Glu Trp Leu Ala Lys Arg Gln Gly Ala Arg Tyr Val Trp Asn Arg
260 265 270

Thr Glu Leu Met Gln Ala Ser Leu Asp Pro Ser Val Thr His Leu Met

275	280	285
Gly Leu Phe Glu Pro Gly Asp Met Lys Tyr Glu Ile His Arg Asp Ser		
290	295	300
Thr Leu Asp Pro Ser Leu Met Glu Met Thr Glu Ala Ala Leu Arg Leu		
305	310	315
320		
Leu Ser Arg Asn Pro Arg Gly Phe Phe Leu Phe Val Glu Gly Gly Arg		
325	330	335
Ile Asp His Gly His His Glu Ser Arg Ala Tyr Arg Ala Leu Thr Glu		
340	345	350
Thr Ile Met Phe Asp Asp Ala Ile Glu Arg Ala Gly Gln Leu Thr Ser		
355	360	365
Glu Glu Asp Thr Leu Ser Leu Val Thr Ala Asp His Ser His Val Phe		
370	375	380
Ser Phe Gly Gly Tyr Pro Leu Arg Gly Ser Ser Ile Phe Gly Leu Ala		
385	390	395
400		
Pro Gly Lys Ala Arg Asp Arg Lys Ala Tyr Thr Val Leu Leu Tyr Gly		
405	410	415
Asn Gly Pro Gly Tyr Val Leu Lys Asp Gly Ala Arg Pro Asp Val Thr		
420	425	430
Glu Ser Glu Ser Gly Ser Pro Glu Tyr Arg Gln Gln Ser Ala Val Pro		
435	440	445
Leu Asp Glu Glu Thr His Ala Gly Glu Asp Val Ala Val Phe Ala Arg		
450	455	460
Gly Pro Gln Ala His Leu Val His Gly Val Gln Glu Gln Thr Phe Ile		
465	470	475
480		
Ala His Val Met Ala Phe Ala Ala Cys Leu Glu Pro Tyr Thr Ala Cys		
485	490	495
Asp Leu Ala Pro Pro Ala Gly Thr Thr Asp Ala Ala His Pro Gly Arg		
500	505	510
Ser Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu		
515	520	525
Leu Glu Thr Ala Thr Ala Pro		
530	535	
<210> 52		
<211> 22		
<212> PRT		
<213> Homo sapiens		
<400> 52		
Met Leu Gly Pro Cys Met Leu Leu Leu Leu Leu Leu Gly Leu Arg		
1	5	10
15		

Leu Gln Leu Ser Leu Gly
20

<210> 53
<211> 29
<212> PRT
<213> Homo sapiens

<400> 53

Ala Ala His Pro Gly Arg Ser Val Val Pro Ala Leu Leu Pro Leu Leu
1 5 10 15

Ala Gly Thr Leu Leu Leu Glu Thr Ala Thr Ala Pro
20 25

<210> 54
<211> 108
<212> PRT
<213> Homo sapiens

<400> 54

Gly Met Gly Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln
1 5 10 15

Lys Lys Asp Lys Leu Gly Pro Glu Ile Pro Leu Ala Met Asp Arg Phe
20 25 30

Pro Tyr Val Ala Leu Ser Lys Thr Tyr Asn Val Asp Lys His Val Pro
35 40 45

Asp Ser Gly Ala Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Gly Asn
50 55 60

Phe Gln Thr Ile Gly Leu Ser Ala Ala Ala Arg Phe Asn Gln Cys Asn
65 70 75 80

Thr Thr Arg Gly Asn Glu Val Ile Ser Val Met Asn Arg Ala Lys Lys
85 90 95

Ala Gly Lys Ser Val Gly Val Val Thr Thr Thr Arg
100 105

<210> 55
<211> 20
<212> PRT
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<220>
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<222> (8)..(8)
<223> "Xaa" may be any amino acid

<400> 55

Ala Gln Val Pro Asp Ser Ala Xaa Thr Ala Thr Ala Tyr Leu Cys Gly
1 5 10 15

Val Lys Ala Asn
20

<210> 56
<211> 86
<212> PRT
<213> Artificial sequence

<220>
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<222> ()..()
<223> Synthetic

<220>
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<222> (7)..(7)
<223> "Xaa" may be any amino acid

<220>
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<222> (30)..(30)
<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
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<222> (36)..(36)
<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
<221> misc_feature
<222> (47)..(47)
<223> "Xaa" may be any amino acid

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<220>
<221> misc_feature
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<223> "Xaa" may be any amino acid

<220>
<221> misc_feature
<222> (65)..(65)
<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<400> 56

Thr Asn Val Ala Lys Asn Xaa Ile Met Phe Leu Gly Asp Gly Met Gly
1 5 10 15

Val Ser Thr Val Thr Ala Ala Arg Ile Leu Lys Gly Gln Xaa His His
20 25 30

Xaa Xaa Gly Xaa Glu Thr Xaa Leu Xaa Met Asp Xaa Phe Pro Xaa Val
35 40 45

Ala Leu Ser Lys Thr Tyr Asn Xaa Xaa Ala Gln Val Pro Asp Ser Ala
50 55 60

Xaa Thr Ala Thr Ala Tyr Leu Cys Gly Val Lys Ala Asn Xaa Xaa Thr
65 70 75 80

Xaa Gly Xaa Ser Ala Ala
85

<210> 57
<211> 53
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<223> "Xaa" may be any amino acid
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<223> "Xaa" may be any amino acid

<220>
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<223> "Xaa" may be any amino acid

<220>
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<222> (34)..(35)
<223> "Xaa" may be any amino acid

<220>
<221> misc_feature
<222> (41)..(42)
<223> "Xaa" may be any amino acid

<400> 57

Glu Asp Thr Leu Thr Xaa Val Thr Ala Asp His Ser His Val Phe Xaa
1           5          10          15

Phe Gly Gly Tyr Thr Xaa Arg Gly Asn Ser Ile Phe Gly Leu Ala Pro
20          25          30

Met Xaa Xaa Asp Thr Asp Lys Lys Xaa Xaa Thr Ala Ile Leu Tyr Gly
35          40          45

Asn Gly Pro Gly Tyr
50

<210> 58
<211> 22
<212> PRT
<213> Homo sapiens

<400> 58

Val Val Pro Ala Leu Leu Pro Leu Leu Ala Gly Thr Leu Leu Leu
1           5          10          15

Glu Thr Ala Thr Ala Pro
20

<210> 59
<211> 154
<212> PRT
<213> Homo sapiens

<400> 59

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1           5          10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
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20

25

30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
 130 135 140

Arg Gly Lys Gly Cys Asp Lys Pro Arg Arg
 145 150

<210> 60

<211> 162

<212> PRT

<213> Artificial sequence

<220>

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<222> ()...()

<223> Synthetic

<400> 60

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Cys Asp Lys Pro
 145 150 155 160

Arg Arg

<210> 61
 <211> 150
 <212> PRT
 <213> Artificial sequence

<220>
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 <222> ()...()
 <223> Synthetic

<400> 61

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys Lys
 130 135 140

Cys Asp Lys Pro Arg Arg
 145 150

<210> 62
 <211> 154
 <212> PRT
 <213> Artificial sequence

<220>

<221> misc_feature
 <222> ()...()
 <223> Synthetic

<400> 62

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Lys
 130 135 140

Lys Lys Lys Cys Asp Lys Pro Arg Arg
 145 150

<210> 63
 <211> 7
 <212> PRT
 <213> Artificial sequence

<220>
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 <222> ()...()
 <223> Synthetic

<400> 63

Gly Gly Gly Gly Ser Ser Ser
 1 5

<210> 64
 <211> 4
 <212> PRT
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()...()

<223> Synthetic

<400> 64

Ile Glu Gly Arg
1

<210> 65

<211> 9

<212> PRT

<213> Artificial sequence

<220>

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<222> ()..()

<223> Synthetic

<400> 65

Pro Gly Ile Ser Gly Gly Gly Gly
1 5

<210> 66

<211> 15

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 66

Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser
1 5 10 15

<210> 67

<211> 13

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 67

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Lys Glu Phe
1 5 10

<210> 68

<211> 26

<212> PRT

<213> Homo sapiens

<400> 68

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Val Leu His His Ala Lys Trp Ser Gln Ala
 20 25

<210> 69
<211> 33
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 69
cgccggatcca ccatgaactt tctgctgtct tgg

33

<210> 70
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 70
ctaaatggtt tctcttcctc cccgcctcgg cttgtcaca

39

<210> 71
<211> 39
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 71
tgtgacaagc ctgaggcggg aggaagagaa accattnag

39

<210> 72
<211> 28
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 72
cgccggatcct caaaaatcta aaggtcga

28

<210> 73

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<211> 1107
<212> DNA
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<220>
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<222> ()..()
<223> Synthetic

<400> 73
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cctgatgaga tcgagttacat cttcaagcca atgaactttc tgctgtctt ggtgcattgg      180
agccttgccct tgctgctcta cctccaccat gccaaagtggt cccagtcctg tgtgcccctg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg ggaggaagag aaaccattta gagactgtgc agatgtatat      480
caagctggtt ttaataaaag tggaatctac actatttata ttaataatat gccagaaccc      540
aaaaaggtgt tttgcaatat ggatgtcaat gggggaggtt ggactgtaat acaacatcgt      600
gaagatggaa gtctagattt ccaaagaggc tggaaaggat ataaaatggg ttttggaaat      660
ccctccggtg aatattggct gggaaatgag tttattttg ccattaccag tcagaggcag      720
tacatgctaa gaattgagtt aatggactgg gaaggaaacc gagccttattc acagtatgac      780
agattccaca taggaaatga aaagcaaaac tataggttgt attaaaagg tcacactggg      840
acagcaggaa aacagagcag cctgatctt cacggtgctg atttcagcac taaagatgt      900
gataatgaca actgtatgtg caaatgtgcc ctcatgttaa caggaggatg gtggtttgat      960
gcttggtggcc cctccaatct aaatggaatg ttctatactg cgggacaaaaa ccatggaaaa      1020
ctgaatggga taaaatggca ctacttcaaa gggcccagtt actccttacg ttccacaact      1080
atgatgattc gacctttaga ttttga                                         1107

<210> 74
<211> 368
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 74

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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140

Pro Arg Arg Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr
 145 150 155 160

Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn
 165 170 175

Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly
 180 185 190

Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln
 195 200 205

Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu
 210 215 220

Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln
 225 230 235 240

Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr
 245 250 255

Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg
 260 265 270

Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu
 275 280 285

Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn
 290 295 300

Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp

305	310	315	320
Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln			
325		330	335
Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro			
340		345	350
Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe			
355	360	365	
<210> 75			
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<400> 75			
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<211> 39			
<212> DNA			
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<220>			
<221> misc_feature			
<222> ()..()			
<223> Synthetic			
<400> 76			
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<210> 77			
<211> 28			
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<213> Artificial sequence			
<220>			
<221> misc_feature			
<222> ()..()			
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<400> 77			
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<222> ()..()			
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gtgaaggttca tggatgtctta tcagcgcagc tactgccatc caatcgagac cctgggtggac 180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tggccctg 240
atgcgatgcg ggggctgctg caatgacgag gcctggagt gtgtgcccac tgaggagtcc 300
aacatcacca tgcagattat gcgatcaaa ctcacccaag gccagcacat aggagagatg 360
agcttcctac agcacaacaa atgtaatgc agaccaaaga aagatagagc aagacaagaa 420
aatgtgaca agccgaggcg gcaatttggc gcggagtgca aataccagtt ccaggcctgg 480
ggagaatgtg acctgaacac agccctgaag accagaactg gaagtctgaa gcgagccctg 540
cacaatgccg aatgccagaa gactgtcacc atctccaagc cctgtggcaa actgaccaag 600
ccccaaacctc aagcagaatc taagaagaag aaaaaggaag gcaagaaaca ggagaagatg 660
ctqqattaa 669

<210> 79

<211> 222

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> () . . ()

<223> Synthetic

<400> 79

Met	Asn	Phe	Leu	Leu	Ser	Trp	Val	His	Trp	Ser	Leu	Ala	Leu	Leu	Leu
1				5					10					15	

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140

Pro Arg Arg Gln Phe Gly Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp
 145 150 155 160

Gly Glu Cys Asp Leu Asn Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu
 165 170 175

Lys Arg Ala Leu His Asn Ala Glu Cys Gln Lys Thr Val Thr Ile Ser
 180 185 190

Lys Pro Cys Gly Lys Leu Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys
 195 200 205

Lys Lys Lys Lys Glu Gly Lys Lys Gln Glu Lys Met Leu Asp
 210 215 220

<210> 80

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()...()

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<400> 80

tgcagtcggc tccaaactcc cgccctcggt tgtcaca

37

<210> 81

<211> 37

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()...()

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<400> 81

tgtgacaaggc cgaggcggga gtttggagcc gactgca

37

<210> 82

<211> 27

<212> DNA

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()...()

<223> Synthetic

<400> 82

cgcggatccc tagtccttcc ccttccc

27

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<210> 83
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<212> DNA
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<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 83
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gtgaagttca tggatgtota tcagcgac tactgccatc caatcgagac cctggtggac      180
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg      240
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc      300
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg      360
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa      420
aaatgtgaca agccgaggcg ggagtttggc gcccactgca agtacaagtt tgagaactgg      480
ggtgcggtgt atgggggcac aggcaccaaa gtccgccaag gcaccctgaa gaaggcgccg      540
tacaatgctc agtgcagga gaccatccgc gtcaccaagc cctgcacccc caagaccaaa      600
gcaaaggcca aagccaagaa agggaaaggga aaggactag                                639

<210> 84
<211> 212
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 84

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1           5           10          15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20          25          30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35          40          45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50          55          60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

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65	70	75	80
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Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro			
85	90	95	

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His			
100	105	110	

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys			
115	120	125	

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys			
130	135	140	

Pro Arg Arg Glu Phe Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp			
145	150	155	160

Gly Ala Cys Asp Gly Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu			
165	170	175	

Lys Lys Ala Arg Tyr Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr			
180	185	190	

Lys Pro Cys Thr Pro Lys Thr Lys Ala Lys Ala Lys Lys Gly			
195	200	205	

Lys Gly Lys Asp
210

<210> 85
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
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36

<210> 86
<211> 36
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
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<400> 86
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36

<210> 87
<211> 28
<212> DNA
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<221> misc_feature		
<222> ()..()		
<223> Synthetic		
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gtgaagttca tggatgtctta tcagcgcagc tactgccatc caatcgagac cctgggtggac	180	
atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg	240	
atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc	300	
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg	360	
agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa	420	
aaatgtgaca agccgaggcg gaagccgtcg ggcccatggaa gagactgcct gcaggccctg	480	
gaggatggcc acgacaccag ctccatctac ctggtaagc cgagaaacac caaccgcctc	540	
atgcaggtgt ggtgcgacca gagacacgac cccgggggct ggaccgtcat ccagagacgc	600	
ctggatggct ctgttaactt cttcaggaac tggagacgt acaagcaagg gtttgggaac	660	
attgatggcg aataactggct gggcctggag aacatttact ggctgacgaa ccaaggcaac	720	
tacaaactcc tggtgaccat ggaggactgg tccggccgca aagtcttgc agaatacgcc	780	
agtttccgccc tggAACCTGA gagcgagtat tataagctgc ggctggggcg ctaccatggc	840	
aatgcgggtg actccttac atggcacaac ggcaagcagt tcaccaccct ggacagagat	900	
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tgtgcccact ccaacctcaa cggggctgg taccgcgggg gccattaccg gagccgctac	1020	
caggacggag tctactgggc tgagttccga ggaggctctt actcactcaa gaaagtggtg	1080	
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<210> 89		

<211> 371
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()...()
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<400> 89

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu
145 150 155 160

Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn
165 170 175

Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly
180 185 190

Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe
195 200 205

Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu
210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn
225 230 235 240

Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe
245 250 255

Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys
 260 265 270

Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp
 275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr
 290 295 300

Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala
 305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
 325 330 335

Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly
 340 345 350

Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn
 355 360 365

Thr Phe His
 370

<210> 90

<211> 36

<212> DNA

<213> Artificial sequence

<220>

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<223> Synthetic

<400> 90

gaatggtcct tcattgatcc gcctcggctt gtcaca

36

<210> 91

<211> 36

<212> DNA

<213> Artificial sequence

<220>

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<223> Synthetic

<400> 91

tgtgacaagc cgaggcggat caatgaagga ccattc

36

<210> 92

<211> 29

<212> DNA

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<222>	()..()						
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gccaa	gttgttgc	cccaggctgc	acccatggca	gaaggaggag	ggcagaatca	tcacgaagt	120
gtgaagttca	tggatgtcta	tcagcgc	gac	tactgccatc	caatcgagac	cctgg	180
atcttccagg	agtaccctga	tgagatcgag	tacatcttca	agccatcctg	tgtgccc	ctg	240
atgcgatgcg	ggggctgctg	caatgacgag	ggcctgg	gtgtgccc	tgaggagt	cc	300
aacatcacca	tgcagattat	gcggatcaaa	cctcacca	gccagcacat	aggagagat	g	360
agcttcctac	agcacaacaa	atgtgaatgc	agaccaa	aagatagagc	aagacaagaa	aa	420
aaatgtgaca	agccgaggcg	gatcaatgaa	ggaccatt	aagactgt	gcaagcaaaa	aa	480
gaagctgggc	attcggtcag	tggatttat	atgattaa	ctgaaa	caatgg	acc	540
atgcagttat	ggtgtaaaa	cagttggac	cctgggg	ggactgtt	tcagaaa	aga	600
acagacggct	ctgtcaactt	cttcagaa	tggaaa	ataagaa	gtttggaa	ac	660
attgacggag	aatactggct	tggactggaa	aatatctata	tgcttagcaa	tcaagata	at	720
tacaagttat	tgattgaatt	agaagactgg	agtataaaa	aagtctatgc	agaata	ac	780
agcttcgtc	tggAACCTGA	aagtgaattc	tatagactgc	gcctgg	ttaccagg	gg	840
aatgcagggg	attctatgat	gtggcata	ggtaaaca	tcaccac	ggacagag	at	900
aaagatatgt	atgcaggaaa	ctgc	ccccac	tttcataa	gaggctgg	gtacaat	960
tgtgcacatt	ctaacctaaa	tggagtatgg	tacagaggag	gccattac	aagcaag	gc	1020
caagatggaa	tttctggc	cgaatacaga	ggcgggt	cat	actc	ccttaa	1080
atgatgatca	agcctattga	ctga					1104
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<221> misc_feature
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<400> 94
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Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
 1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
 20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
 130 135 140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
 145 150 155 160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
 165 170 175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
 180 185 190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
 195 200 205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
 210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
 225 230 235 240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp. Trp Ser Asp Lys Lys Val Tyr
 245 250 255

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg
 260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp
 275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr			
290	295	300	
Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala			
305	310	315	320
Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr			
325	330	335	
Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly			
340	345	350	
Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp			
355	360	365	
<210> 95			
<211> 1387			
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<223> "n" may be any nucleotide			
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<223> "n" may be any nucleotide			
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aactttcgga agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc		120	
tgcagctaca ctttcctcct gccagagatg gacaactgcc gctttcctc cagcccctac		180	
gtgtccaatg ctgtgcagag ggacgcgcgg ctcgaatacg atgactcggt gcagaggctg		240	
caagtgctgg agaacatcat ggaaaacaac actcagtgcc taatgaaggt agagaatata		300	
tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag		360	
acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcggg gcaaacgcgg		420	
aagttaactg atgtggaagc ccaagtatta aatcagacca cgagacttga acttcagctc		480	
ttggaacact ccctctcgac aaacaaattg gaaaaacaga ttttggacca gaccagtgaa		540	
ataaaacaaat tgcaagataa gaacagttc ctagaaaaga aggtgcttagc tatggaagac		600	
aagcacatca tccaactaca gtcaataaaa gaagagaaaag atcagctaca ggtgttagta		660	

tccaaggcaga	attccatcat	tgaagaactc	aaaaaaaaaa	tagtgactgc	cacggtaat	720
aattcagttc	ttcagaagca	gcaacatgat	ctcatggaga	cagttaataa	cttactgact	780
atgatgtcca	catcaaacgc	agctaaggac	cccactgtt	ctaaagaaga	acaaatcagc	840
ttcagagact	gtgctgaagt	attcaaatca	ggacacacca	cgaatggcat	ctacacgtta	900
acattcccta	attctacaga	agagatcaag	gcctactgt	acatggaagc	tggaggaggc	960
gggtggacaa	ttattcagcg	acgtgaggat	ggcagcgtt	catttcagag	gacttggaaa	1020
gaatataaag	tgggatttgg	taacctctca	aaaaaatatt	ggctggaaa	tgagtttgg	1080
tcgcaactga	ctaattcagca	acgctatgt	cttaaaatac	accttaaaga	ctgggaaggg	1140
aatgaggctt	actcattgta	tgaacatttc	tatctctcaa	gtgaagaact	caattatagg	1200
nnnnnnnnnn	nnnnnnnnng	gcaatgattt	tagcacaagg	gatggagcca	ccgnncanatg	1260
tatttgcaaa	tgttcacaaa	tgctaacagn	aggtnnnnnn	nnnnnnnnnn	nnnnnnnnnn	1320
nnnntactgg	aaaggctcag	gctattcgct	caaggccaca	accatgatga	tccgaccagc	1380
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<210> 96
<211> 360
<212> PRT
<213> Artificial sequence

<220>
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<220>
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<222> (269)..(272)
<223> "Xaa" may be any amino acid

<400> 96

Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala
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Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys
20 25 30

Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro
35 40 45

Glu Met Asp Asn Cys Arg Ser Ser Ser Pro Tyr Val Ser Asn Ala
50 55 60

Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val Gln Arg Leu
65 70 75 80

Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp Leu Met Lys

85

90

95

Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
 100 105 110

Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
 115 120 125

Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
 130 135 140

Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu Glu Leu Gln Leu
 145 150 155 160

Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
 165 170 175

Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
 180 185 190

Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
 195 200 205

Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
 210 215 220

Ser Ile Ile Glu Glu Leu Glu Lys Ile Val Thr Ala Thr Val Asn
 225 230 235 240

Asn Ser Val Leu Gln Lys Gln His Asp Leu Met Glu Thr Val Asn
 245 250 255

Asn Leu Leu Thr Met Met Ser Thr Ser Asn Cys Lys Xaa Xaa Xaa Xaa
 260 265 270

Val Ala Lys Glu Glu Gln Ile Ser Phe Arg Asp Cys Ala Glu Val Phe
 275 280 285

Lys Ser Gly His Thr Thr Asn Gly Ile Tyr Thr Leu Met Trp Gln Ile
 290 295 300

Val Phe Phe Thr Leu Ser Cys Asp Leu Val Leu Ala Ala Ala Tyr Asn
 305 310 315 320

Asn Phe Arg Lys Ser Met Asp Ser Ile Gly Lys Lys Gln Tyr Gln Val
 325 330 335

Gln His Gly Ser Cys Ser Tyr Thr Phe Leu Leu Pro Glu Met Asp Asn
 340 345 350

Cys Arg Ser Ser Ser Pro Tyr
 355 360

<210> 97

<211> 339

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 97

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg Met Pro Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val
145 150 155 160

Asn Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu
165 170 175

Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro
180 185 190

Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser
195 200 205

Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn
210 215 220

Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln
225 230 235 240

Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln
245 250 255

Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp
260 265 270

Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp
275 280 285

Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr
 290 295 300

Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe
 305 310 315 320

Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro
 325 330 335

Leu Asp Phe

<210> 98
<211> 361
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
<223> Synthetic

<400> 98
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agtgctggag aacatcatgg aaaacaacac tcagtggcta atgaaggtag agaatatatc
ccaggacaac atgaagaaag aaatggtaga gatacagcag aatgcagtac agaaccagac 120
ggctgtatg atagaaatag ggacaaacct gttgaaccaa acagcggagc aaacgcggaa 180
gttaactgat gtggaagccc aagtattaaa tcagaccacg agacttgaac ttcagcttt 240
ggaacactcc ctctcgacaa acaaattgga aaaacagatt ttggaccaga ccagtgaaat 300
a 360

<210> 99
<211> 123
<212> PRT
<213> Artificial sequence

<220>
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<223> Synthetic

<400> 99

Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser
 1 5 10 15

Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln
 20 25 30

Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu
 35 40 45

Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met

50	55	60
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg		
65	70	75
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu		
85	90	95
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys		
100	105	110
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys		
115	120	
<210> 100		
<211> 462		
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<220>		
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<222> ()...()		
<223> Synthetic		
<400> 100		
Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser		
1	5	10
15		
Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln		
20	25	30
Trp Leu Met Lys Leu Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu		
35	40	45
Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met		
50	55	60
Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg		
65	70	75
80		
Lys Leu Thr Asp Val Glu Ala Gln Val Ser Asn Ala Thr Thr Arg Leu		
85	90	95
Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys		
100	105	110
Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Met Asn Phe Leu Leu		
115	120	125
Ser Trp Val His Trp Ser Leu Ala Leu Leu Tyr Leu His His Ala		
130	135	140
Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gln Asn His		
145	150	155
160		
His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His		
165	170	175

Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile
 180 185 190
 Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly
 195 200 205
 Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn
 210 215 220
 Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile
 225 230 235 240
 Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys
 245 250 255
 Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg Arg Met Pro
 260 265 270
 Glu Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Trp
 275 280 285
 Thr Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly
 290 295 300
 Trp Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp
 305 310 315 320
 Leu Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met
 325 330 335
 Leu Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln
 340 345 350
 Tyr Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr
 355 360 365
 Leu Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu
 370 375 380
 His Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asn Cys Met
 385 390 395 400
 Cys Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys
 405 410 415
 Gly Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His
 420 425 430
 Gly Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr
 435 440 445
 Ser Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
 450 455 460
 <210> 101
 <211> 224
 <212> PRT
 <213> Homo sapiens

<400> 101

Lys	Pro	Ser	Gly	Pro	Trp	Arg	Asp	Cys	Leu	Gln	Ala	Leu	Glu	Asp	Gly
1				5					10				15		

His	Asp	Thr	Ser	Ser	Ile	Tyr	Leu	Val	Lys	Pro	Glu	Asn	Thr	Asn	Arg
				20				25				30			

Leu	Met	Gln	Val	Trp	Cys	Asp	Gln	Arg	His	Asp	Pro	Gly	Gly	Trp	Thr
					35		40				45				

Val	Ile	Gln	Arg	Arg	Leu	Asp	Gly	Ser	Val	Asn	Phe	Phe	Arg	Asn	Trp
				50			55			60					

Glu	Thr	Tyr	Lys	Gln	Gly	Phe	Gly	Asn	Ile	Asp	Gly	Glu	Tyr	Trp	Leu
				65		70			75			80			

Gly	Leu	Glu	Asn	Ile	Tyr	Trp	Leu	Thr	Asn	Gln	Gly	Asn	Tyr	Lys	Leu
				85				90			95				

Leu	Val	Thr	Met	Glu	Asp	Trp	Ser	Gly	Arg	Lys	Val	Phe	Ala	Glu	Tyr
			100				105				110				

Ala	Ser	Phe	Arg	Leu	Glu	Pro	Glu	Ser	Glu	Tyr	Tyr	Lys	Leu	Arg	Leu
				115			120			125					

Gly	Arg	Tyr	His	Gly	Asn	Ala	Gly	Asp	Ser	Phe	Thr	Trp	His	Asn	Gly
			130			135				140					

Lys	Gln	Phe	Thr	Thr	Leu	Asp	Arg	Asp	His	Asp	Val	Tyr	Thr	Gly	Asn
				145		150			155			160			

Cys	Ala	His	Tyr	Gln	Lys	Gly	Gly	Trp	Trp	Tyr	Asn	Ala	Cys	Ala	His
				165			170			175					

Ser	Asn	Leu	Asn	Gly	Val	Trp	Tyr	Arg	Gly	Gly	His	Tyr	Arg	Ser	Arg
				180			185				190				

Tyr	Gln	Asp	Gly	Val	Tyr	Trp	Ala	Glu	Phe	Arg	Gly	Gly	Ser	Tyr	Ser
				195			200			205					

Leu	Lys	Lys	Val	Val	Met	Met	Ile	Arg	Pro	Asn	Pro	Asn	Thr	Phe	His
				210			215				220				

<210> 102

<211> 220

<212> PRT

<213> Homo sapiens

<400> 102

Ile	Asn	Glu	Gly	Pro	Phe	Lys	Asp	Cys	Gln	Gln	Ala	Lys	Glu	Ala	Gly
1					5				10			15			

His	Ser	Val	Ser	Gly	Ile	Tyr	Met	Ile	Lys	Pro	Glu	Asn	Ser	Asn	Gly
					20			25			30				

Pro	Met	Gln	Leu	Trp	Cys	Glu	Asn	Ser	Leu	Asp	Pro	Gly	Gly	Trp	Thr
				35			40				45				

Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe Arg Asn Trp
50 55 60

Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu
65 70 75 80

Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn Tyr Lys Leu
85 90 95

Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr Ala Glu Tyr
100 105 110

Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg Leu Arg Leu
115 120 125

Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp His Asn Gly
130 135 140

Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr Ala Gly Asn
145 150 155 160

Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His
165 170 175

Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Lys
180 185 190

His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Ser Tyr Ser
195 200 205

Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
210 215 220

<210> 103

<211> 371

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 103

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu

65	70	75	80
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro			
85		90	95
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His			
100		105	110
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys			
115		120	125
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys			
130	135	140	
Pro Arg Arg Lys Pro Ser Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu			
145	150	155	160
Glu Asp Gly His Asp Thr Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn			
165		170	175
Thr Asn Arg Leu Met Gln Val Trp Cys Asp Gln Arg His Asp Pro Gly			
180		185	190
Gly Trp Thr Val Ile Gln Arg Arg Leu Asp Gly Ser Val Asn Phe Phe			
195		200	205
Arg Asn Trp Glu Thr Tyr Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu			
210		215	220
Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn			
225		230	235
Tyr Lys Leu Leu Val Thr Met Glu Asp Trp Ser Gly Arg Lys Val Phe			
245		250	255
Ala Glu Tyr Ala Ser Phe Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys			
260		265	270
Leu Arg Leu Gly Arg Tyr His Gly Asn Ala Gly Asp Ser Phe Thr Trp			
275		280	285
His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp His Asp Val Tyr			
290		295	300
Thr Gly Asn Cys Ala His Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala			
305		310	315
Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr			
325		330	335
Arg Ser Arg Tyr Gln Asp Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly			
340		345	350
Ser Tyr Ser Leu Lys Lys Val Val Met Met Ile Arg Pro Asn Pro Asn			
355		360	365
Thr Phe His			
370			

<210> 104
<211> 367
<212> PRT
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()...()
<223> Synthetic

<400> 104

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg Ile Asn Glu Gly Pro Phe Lys Asp Cys Gln Gln Ala Lys
145 150 155 160

Glu Ala Gly His Ser Val Ser Gly Ile Tyr Met Ile Lys Pro Glu Asn
165 170 175

Ser Asn Gly Pro Met Gln Leu Trp Cys Glu Asn Ser Leu Asp Pro Gly
180 185 190

Gly Trp Thr Val Ile Gln Lys Arg Thr Asp Gly Ser Val Asn Phe Phe
195 200 205

Arg Asn Trp Glu Asn Tyr Lys Lys Gly Phe Gly Asn Ile Asp Gly Glu
210 215 220

Tyr Trp Leu Gly Leu Glu Asn Ile Tyr Met Leu Ser Asn Gln Asp Asn
225 230 235 240

Tyr Lys Leu Leu Ile Glu Leu Glu Asp Trp Ser Asp Lys Lys Val Tyr
245 250 255

Ala Glu Tyr Ser Ser Phe Arg Leu Glu Pro Glu Ser Glu Phe Tyr Arg
260 265 270

Leu Arg Leu Gly Thr Tyr Gln Gly Asn Ala Gly Asp Ser Met Met Trp
275 280 285

His Asn Gly Lys Gln Phe Thr Thr Leu Asp Arg Asp Lys Asp Met Tyr
290 295 300

Ala Gly Asn Cys Ala His Phe His Lys Gly Gly Trp Trp Tyr Asn Ala
305 310 315 320

Cys Ala His Ser Asn Leu Asn Gly Val Trp Tyr Arg Gly Gly His Tyr
325 330 335

Arg Ser Lys His Gln Asp Gly Ile Phe Trp Ala Glu Tyr Arg Gly Gly
340 345 350

Ser Tyr Ser Leu Arg Ala Val Gln Met Met Ile Lys Pro Ile Asp
355 360 365

<210> 105

<211> 53

<212> PRT

<213> Homo sapiens

<400> 105

Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys Lys Glu Met Val Glu
1 5 10 15

Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile
20 25 30

Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr
35 40 45

Asp Val Glu Ala Gln
50

<210> 106

<211> 105

<212> PRT

<213> Homo sapiens

<400> 106

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
1 5 10 15

Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
20 25 30

Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
35 40 45

Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys
100 105

<210> 107

<211> 192

<212> PRT

<213> Homo sapiens

<400> 107

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro
180 185 190

<210> 108

<211> 196

<212> PRT

<213> Homo sapiens

<400> 108

Pro Tyr Val Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp
 1 5 10 15

Asp Ser Val Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn
 20 25 30

Thr Gln Trp Leu Met Lys Leu Glu Asn Tyr Ile Gln Asp Asn Met Lys
 35 40 45

Lys Glu Met Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala
 50 55 60

Val Met Ile Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln
 65 70 75 80

Thr Arg Lys Leu Thr Asp Val Glu Ala Gln Val Leu Asn Gln Thr Thr
 85 90 95

Arg Leu Glu Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu
 100 105 110

Glu Lys Gln Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp
 115 120 125

Lys Asn Ser Phe Leu Glu Lys Lys Val Leu Ala Met Glu Asp Lys His
 130 135 140

Ile Ile Gln Leu Gln Ser Ile Lys Glu Glu Lys Asp Gln Leu Gln Val
 145 150 155 160

Leu Val Ser Lys Gln Asn Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile
 165 170 175

Val Thr Ala Thr Val Asn Asn Ser Val Leu Gln Lys Gln Gln His Asp
 180 185 190

Leu Met Glu Thr
 195

<210> 109

<211> 105

<212> PRT

<213> Homo sapiens

<400> 109

His Gly Leu Leu Gln Leu Gly Gln Gly Leu Arg Glu His Ala Glu Arg
 1 5 10 15

Thr Arg Ser Gln Leu Ser Ala Leu Glu Arg Arg Leu Ser Ala Cys Gly
 20 25 30

Ser Ala Cys Gln Gly Thr Glu Gly Ser Thr Asp Leu Pro Leu Ala Pro
 35 40 45

Glu Ser Arg Val Asp Pro Glu Val Leu His Ser Leu Gln Thr Gln Leu
 50 55 60

Lys Ala Gln Asn Ser Arg Ile Gln Gln Leu Phe His Lys Val Ala Gln
65 70 75 80

Gln Gln Arg His Leu Glu Lys Gln His Leu Arg Ile Gln His Leu Gln
85 90 95

Ser Gln Phe Gly Leu Leu Asp His Lys
100 105

<210> 110

<211> 192

<212> PRT

<213> Homo sapiens

<400> 110

Gly Pro Ile Cys Val Asn Thr Lys Gly Gln Asp Ala Ser Thr Ile Lys
1 5 10 15

Asp Met Ile Thr Arg Met Asp Leu Glu Asn Leu Lys Asp Val Leu Ser
20 25 30

Arg Gln Lys Arg Glu Ile Asp Val Leu Gln Leu Val Val Asp Val Asp
35 40 45

Gly Asn Ile Val Asn Glu Val Lys Leu Leu Arg Lys Glu Ser Arg Asn
50 55 60

Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu Ile
65 70 75 80

Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu Ser Gln Leu Glu Asn Lys
85 90 95

Ile Leu Asn Val Thr Thr Glu Met Leu Lys Met Ala Thr Arg Tyr Arg
100 105 110

Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr Asp Leu Val Asn Asn Gln
115 120 125

Ser Val Met Ile Thr Leu Leu Glu Glu Gln Cys Leu Arg Ile Phe Ser
130 135 140

Arg Gln Asp Thr His Val Ser Pro Pro Leu Val Gln Val Val Pro Gln
145 150 155 160

His Ile Pro Asn Ser Gln Gln Tyr Thr Pro Gly Leu Leu Gly Gly Asn
165 170 175

Glu Ile Gln Arg Asp Pro Gly Tyr Pro Arg Asp Leu Met Pro Pro Pro
180 185 190

<210> 111

<211> 135

<212> PRT

<213> Homo sapiens

<400> 111

Asp Ala Ser Thr Ile Lys Asp Met Ile Thr Arg Met Asp Leu Glu Asn
1 5 10 15

Leu Lys Asp Val Leu Ser Arg Gln Lys Arg Glu Ile Asp Val Leu Gln
20 25 30

Leu Val Val Asp Val Asp Gly Asn Ile Val Asn Glu Val Lys Leu Leu
35 40 45

Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met
50 55 60

Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn Ser Leu Glu Leu
65 70 75 80

Ser Gln Leu Glu Asn Lys Ile Leu Asn Val Thr Thr Glu Met Leu Lys
85 90 95

Met Ala Thr Arg Tyr Arg Glu Leu Glu Val Lys Tyr Ala Ser Leu Thr
100 105 110

Asp Leu Val Asn Asn Gln Ser Val Met Ile Thr Leu Leu Glu Glu Gln
115 120 125

Cys Leu Arg Ile Phe Ser Arg
130 135

<210> 112

<211> 101

<212> PRT

<213> Homo sapiens

<400> 112

Glu Leu Glu Leu Leu Asn Asn Glu Leu Leu Lys Gln Lys Arg Gln Ile
1 5 10 15

Glu Thr Leu Gln Gln Leu Val Glu Val Asp Gly Gly Ile Val Ser Glu
20 25 30

Val Lys Leu Leu Arg Lys Glu Ser Arg Asn Met Asn Ser Arg Val Thr
35 40 45

Gln Leu Tyr Met Gln Leu Leu His Glu Ile Ile Arg Lys Arg Asp Asn
50 55 60

Ala Leu Glu Leu Ser Gln Leu Glu Asn Arg Ile Leu Asn Gln Thr Ala
65 70 75 80

Asp Met Leu Gln Leu Ala Ser Lys Tyr Lys Asp Leu Glu His Lys Tyr
85 90 95

Gln His Leu Ala Thr
100

<210> 113

<211> 493

<212> PRT

<213> Homo sapiens

<400> 113

Met Arg Pro Leu Cys Val Thr Cys Trp Trp Leu Gly Leu Leu Ala Ala
1 5 10 15

Met Gly Ala Val Ala Gly Gln Glu Asp Gly Phe Glu Gly Thr Glu Glu
20 25 30

Gly Ser Pro Arg Glu Phe Ile Tyr Leu Asn Arg Tyr Lys Arg Ala Gly
35 40 45

Glu Ser Gln Asp Lys Gys Thr Tyr Thr Phe Ile Val Pro Gln Gln Arg
50 55 60

Val Thr Gly Ala Ile Cys Val Asn Ser Lys Glu Pro Glu Val Leu Leu
65 70 75 80

Glu Asn Arg Val His Lys Gln Glu Leu Glu Leu Leu Asn Asn Glu Leu
85 90 95

Leu Lys Gln Lys Arg Gln Ile Glu Thr Leu Gln Gln Leu Val Glu Val
100 105 110

Asp Gly Gly Ile Val Ser Glu Val Lys Leu Leu Arg Lys Glu Ser Arg
115 120 125

Asn Met Asn Ser Arg Val Thr Gln Leu Tyr Met Gln Leu Leu His Glu
130 135 140

Ile Ile Arg Lys Arg Asp Asn Ala Leu Glu Leu Ser Gln Leu Glu Asn
145 150 155 160

Arg Ile Leu Asn Gln Thr Ala Asp Met Leu Gln Leu Ala Ser Lys Tyr
165 170 175

Lys Asp Leu Glu His Lys Tyr Gln His Leu Ala Thr Leu Ala His Asn
180 185 190

Gln Ser Glu Ile Ile Ala Gln Leu Glu Glu His Cys Gln Arg Val Pro
195 200 205

Ser Ala Arg Pro Val Pro Gln Pro Pro Pro Ala Ala Pro Pro Arg Val
210 215 220

Tyr Gln Pro Pro Thr Tyr Asn Arg Ile Ile Asn Gln Ile Ser Thr Asn
225 230 235 240

Glu Ile Gln Ser Asp Gln Asn Leu Lys Val Leu Pro Pro Pro Leu Pro
245 250 255

Thr Met Pro Thr Leu Thr Ser Leu Pro Ser Ser Thr Asp Lys Pro Ser
260 265 270

Gly Pro Trp Arg Asp Cys Leu Gln Ala Leu Glu Asp Gly His Asp Thr
275 280 285

Ser Ser Ile Tyr Leu Val Lys Pro Glu Asn Thr Asn Arg Leu Met Gln
290 295 300

Val Trp Cys Asp Gln Arg His Asp Pro Gly Gly Trp Thr Val Ile Gln
305 310 315 320

Arg Arg Leu Asp Gly Ser Val Asn Phe Phe Arg Asn Trp Glu Thr Tyr
325 330 335

Lys Gln Gly Phe Gly Asn Ile Asp Gly Glu Tyr Trp Leu Gly Leu Glu
340 345 350

Asn Ile Tyr Trp Leu Thr Asn Gln Gly Asn Tyr Lys Leu Leu Val Thr
355 360 365

Met Glu Asp Trp Ser Gly Arg Lys Val Phe Ala Glu Tyr Ala Ser Phe
370 375 380

Arg Leu Glu Pro Glu Ser Glu Tyr Tyr Lys Leu Arg Leu Gly Arg Tyr
385 390 395 400

His Gly Asn Ala Gly Asp Ser Phe Thr Trp His Asn Gly Lys Gln Phe
405 410 415

Thr Thr Leu Asp Arg Asp His Asp Val Tyr Thr Gly Asn Cys Ala His
420 425 430

Tyr Gln Lys Gly Gly Trp Trp Tyr Asn Ala Cys Ala His Ser Asn Leu
435 440 445

Asn Gly Val Trp Tyr Arg Gly Gly His Tyr Arg Ser Arg Tyr Gln Asp
450 455 460

Gly Val Tyr Trp Ala Glu Phe Arg Gly Gly Ser Tyr Ser Leu Lys Lys
465 470 475 480

Val Val Met Met Ile Arg Pro Asn Pro Asn Thr Phe His
485 490

<210> 114

<211> 54

<212> PRT

<213> Homo sapiens

<400> 114

Thr Asn Lys Leu Glu Arg Gln Met Leu Met Gln Ser Arg Glu Leu Gln
1 5 10 15

Arg Leu Gln Gly Arg Asn Arg Ala Leu Glu Thr Arg Leu Gln Ala Leu
20 25 30

Glu Ala Gln His Gln Ala Gln Leu Asn Ser Leu Gln Glu Lys Arg Glu
35 40 45

Gln Leu His Ser Leu Leu
50

<210> 115

<211> 145

<212> PRT

<213> Homo sapiens

<400> 115

Thr	Gln	Gln	Val	Lys	Gln	Leu	Glu	Gln	Ala	Leu	Gln	Asn	Asn	Thr	Gln
1				5				10						15	

Trp	Leu	Lys	Lys	Leu	Glu	Arg	Ala	Ile	Lys	Thr	Ile	Leu	Arg	Ser	Lys
				20				25					30		

Leu	Glu	Gln	Val	Gln	Gln	Met	Ala	Gln	Asn	Gln	Thr	Ala	Pro	Met
				35			40				45			

Leu	Glu	Leu	Gly	Thr	Ser	Leu	Leu	Asn	Gln	Thr	Thr	Ala	Gln	Ile	Arg
				50			55			60					

Lys	Leu	Thr	Asp	Met	Glu	Ala	Gln	Leu	Leu	Asn	Gln	Thr	Ser	Arg	Met
65					70					75			80		

Asp	Ala	Gln	Met	Pro	Glu	Thr	Phe	Leu	Ser	Thr	Asn	Lys	Leu	Glu	Asn
				85				90			95				

Gln	Leu	Leu	Leu	Gln	Arg	Gln	Lys	Leu	Gln	Gln	Leu	Gln	Gly	Gln	Asn
				100				105				110			

Ser	Ala	Leu	Glu	Lys	Arg	Leu	Gln	Ala	Leu	Glu	Thr	Lys	Gln	Gln	Glu
				115				120			125				

Glu	Leu	Ala	Ser	Ile	Leu	Ser	Lys	Lys	Ala	Lys	Leu	Leu	Asn	Thr	Leu
				130			135				140				

Ser
145

<210> 116

<211> 465

<212> DNA

<213> Homo sapiens

<400>	116														60
gccccatggag	agactgcctg	caggccctgg	aggatggcca	cgacaccagc	tccatctacc										

tggtaagcc	ggagaacacc	aaccgcctca	tgcaggtgtg	gtgcgaccag	agacacgacc										120
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ccgggggctg	gaccgtcatc	cagagacgcc	tggatggctc	tgttaacttc	ttcaggaact										180
------------	------------	------------	------------	------------	------------	--	--	--	--	--	--	--	--	--	-----

gggagacgta	caagcaaggg	tttgggaaca	ttgacggcga	atactggctg	ggcctggaga										240
------------	------------	------------	------------	------------	------------	--	--	--	--	--	--	--	--	--	-----

acatttactg	gctgacgaac	caaggcaact	acaaactcct	ggtgaccatg	gaggactggt										300
------------	------------	------------	------------	------------	------------	--	--	--	--	--	--	--	--	--	-----

ccggccgcaa	agtcttgca	gaatacggca	gtttccgcct	ggaacctgag	agcgagtatt										360
------------	-----------	------------	------------	------------	------------	--	--	--	--	--	--	--	--	--	-----

ataagctgctg	gctggggcgc	taccatggca	atgcgggtga	ctcctttaca	tggcacaacg										420
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gcaaggcagtt	caccacccag	gacagagatc	atgatgtcta	cacag											465
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<210> 117

<211> 305

<212> DNA

<213> Homö sapiens

<400> 117
ggattgccag gagctgttcc aggttgggga gaggcagagt ggactattg aaatccagcc 60
tcaggggtct ccgcatttt tggtaactg caagatgacc tcagatggag gctggacagt
aattcagagg cgccacgatg gtcagtgga cttcaaccgg ccctkggtag cctacaaggc 120
ggtggttttggggatcccc acggcgagtt ctggcttggg tcttggagaa aggkgcatag
catcacgggg ggaccggaac agccgmctgg ccgtgcaamc tgcggggact gggatggca 180
300
aacgc 305

<210> 118
<211> 458
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (224)..(244)
<223> "n" may be any nucleotide

<220>
<221> misc_feature
<222> (347)..(347)
<223> "n" may be any nucleotide

<220>
<221> misc_feature
<222> (353)..(353)
<223> "n" may be any nucleotide

<220>
<221> misc_feature
<222> (384)..(384)
<223> "n" may be any nucleotide

<220>
<221> misc_feature
<222> (400)..(400)
<223> "n" may be any nucleotide

<220>
<221> misc_feature
<222> (446)..(446)
<223> "n" may be any nucleotide

<400> 118
attataagct gcggctgggg cgataccatg gcaatgcggg tgactcctt acatggcaca 60
acggcaagca gttcaccacc ctggacagag atcatgatgt ctacacagga aactgtgcc 120
actaccagaa gggaggctgg tggtaataacg cctgtgccc ctcacaccc aaccgggtc 180
tggtaccgcg gggccatTA ccggagccgc taccaggacg gagngtactg ggctgagttc 240

cgaggaggct ttactcact caaggaaacg tggatgtat gatccgaccg aaccccaaca 300
 ccttcacta agccagctcc ccctcctgac ctctccgtgg ccattgnac gangcccacc 360
 ctggtcacgc tggccacagc acanagaaca actcctcactn agttcatcct gaggctggga 420
 ggaccggat gctggattct gtttnccga agtcactg 458

 <210> 119
 <211> 173
 <212> DNA
 <213> Artificial sequence

 <220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

 <400> 119
 tataagctgc ggctggggcg ataccatggc aatgcgggtg actccttac atggcacaac 60
 ggcaagcagt tcaccacocct ggacagagat catgatgtct acacaggaaa ctgtgcccac 120
 taccagaagg gaggctggtg gtataacgcc tgtgccact ccaacctcaa ccg 173

 <210> 120
 <211> 638
 <212> DNA
 <213> Artificial sequence

 <220>
 <221> misc_feature
 <222> ()..()
 <223> Synthetic

 <400> 120
 gccccatggag agactgcctg caggccctgg agatggcca cgacaccagg tccatctacc 60
 tggtaagcc ggagaacacc aaccgcctca tgcagggtgt gtgcgaccag agacacgacc 120
 ccgggggctg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaggaact 180
 gggagacgta caagcaaggg tttggaaaca ttgacggcga atactggctg ggcctggaga 240
 acatttactg gctgacgaac caaggcaact acaaactcct ggtgaccatg gaggactgg 300
 ccggccgcaa agtcttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360
 ataagctgcg gctggggcgc taccatggca atgcgggtga ctcccttaca tggcacaacg 420
 gcaaggcgtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480
 gggcgatacc atggcaatgc gggtaactcc tttacatggc acaacggcaa gcagttcacc 540
 accctggaca gagatcatga tgtctacaca ggaaactgtg cccactacca gaagggaggc 600
 tggtgtata acgcctgtgc ccactccaac ctcaaccg 638

 <210> 121

<211> 4045
<212> DNA
<213> Artificial sequence

<220>
<221> misc_feature
<222> ()..()
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<400> 121
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tggtaagcc ggagaacacc aaccgcctca tgcaggtgtg gtgcgaccag agacacgacc 120
ccggggcgtg gaccgtcatc cagagacgcc tggatggctc tgttaacttc ttcaagaact 180
gggagacgta caagcaaggg tttgggaaca ttgacggcga atactggctg ggcctggaga 240
acatttactg gctgacgaaac caaggcaact acaaactcct ggtgaccatg gaggactgg 300
ccggccgcaa agtctttgca gaatacgcca gtttccgcct ggaacctgag agcgagtatt 360
ataagctgca gctggggcgc taccatggca atgcgggtga ctctttaca tggcacaacg 420
gcaagcagtt caccacccag gacagagatc atgatgtcta cacagtataa gctgcggctg 480
gggcgatacc atggcaatgc gggtaactcc tttacatggc acaacggcaa gcagttcacc 540
accctggaca gagatcatga tgtctacaca ggaaactgtg cccactacca gaagggaggc 600
tggtgtata acgcctgtgc ccactccaaac ctcaaccgga aaaagagagg aagagaaaacc 660
attagagac tgtcagatg tatacaagc tggtttaat aaaagtggaa tctacactat 720
ttatattaat aatatgccag aacccaaaaa ggtgtttgc aatatggatg tcaatggggg 780
aggttggact gtaatacaac atcgtgaaga tggaaagtcta gattccaaa gaggctggaa 840
ggaatataaa atgggttttg gaaatccctc cggtaatat tggctggga atgagttat 900
ttttgccatt accagtcaga ggcagtacat gctaagaatt gagtaatgg actggaaagg 960
gaaccgagcc tattcacagt atgacagatt ccacatagga aatgaaaagc aaaactatag 1020
gttgtattta aaaggtcaca ctgggacagc aggaaaacag agcagcctga tcttacacgg 1080
tgctgatttc agcactaaag atgctgataa tgacaactgt atgtgcaaat gtgcctcat 1140
gttaacagga ggtatgggtt ttgatgcttg tggccctcc aatctaaatg gaatgttcta 1200
tactgcggga caaaaaccatg gaaaactgaa tggataaag tggcactact tcaaaggccc 1260
cagttactcc ttacgttcca caactatgat gattcgacct ttagatttt gaaagcgcaa 1320
tgtcagaagc gattatgaaa gcaacaaaga aatccggaga agctgccagg tgagaaactg 1380
tttggaaaact tcagaagcaa acaatattgt ctcccttcca gcaataagtg gtatgttatgt 1440
gaagtccacca aggttcttga ccgtgaatct ggagccgtt gagttcacaa gagtctctac 1500

ttggggtgac agtgctcacg tggctcgact atagaaaaact ccactgactg tcgggctta	1560
aaaagggaaag aaactgctga gcttgctgtg cttcaaacta ctactggacc ttatTTGGA	1620
actatggtag ccagatgata aatatggta atttcatgta aaacagaaaa aaagagtgaa	1680
aaagagaata tacatgaaga atagaaaaca gcctgccata atccttgga aaagatgtat	1740
tataccagtg aaaaggcgtt atatctatgc aaacctacta acaaattata ctgtgcaca	1800
atTTTgataa aaatTTgaa cagcattgtc ctctgagttg gttaaatgtt aatggatttc	1860
agaaggcctaa ttccagtatc atacttacta gttgatttct gcttacccat cttcaaATGA	1920
aaATTCCATT TTTGTAAGCC ataATGAACT gtagtACATg gacaATAAGT gtGTGGTAGA	1980
aacAAACtCC attactCTGA TTTTGATAc agTTTcAGA AAAAGAAATG AACATAATCA	2040
agtaaggatg tatgtggtaaa acttacca cccccatact atggTTTCA tttactctaa	2100
aaactgattg aatgatatat aaatATATTt atAGCCTGAG taaAGTTAA agaATGAAA	2160
atATATCATC aagttcttaa aataatatac atgcatttaa tattTCCTT gatattatac	2220
aggAAAGCAA TTTTGAGG TATGTTAAGT tgaAGTAAAA CCAAGTACTC TGGAGCAGTT	2280
cattttacag tatctacttg catgtgtata catacatgta acttcattat tttaAAAATA	2340
tttttagAAC TCCAATACTC ACCCTGTTAT GCTTGCTAA TTAAATTtT GCTAATTAAC	2400
TGAAACATGC ttaccagatt cacactgttc cagtgtctat AAAAGAAACA CTTCGAAGTC	2460
tataAAAAAT AAAATAATTa TAAATATCAT TGTACATAGC ATGTTATAT CTGCAAAAAA	2520
CCTAATAGCT aattaATCTG gaatATGCAA CATTGTCCTT AATTGATGCA AATAACACAA	2580
ATGCTCAAAG AAATCTACTA TATCCCTTA TGAATAACAT CATTCTTCAT ATATTCTCC	2640
ttcAGTCCAT TCCCTTAGGC aatttttaat tttaAAAAT tattATCAGG ggagAAAAAT	2700
TGGCAAAACT ATTATATGTA AGGGATATAT ATATAcAAAAG AGAAAATTAA TCAAGTCAC	2760
CTGACTAAGA aattCTGACT GCTAGTTGCC ATAAATAACT CAATGGAAAT ATTCCTATGG	2820
GATAATGTAT TTAAAGTGAa TTTTGGGT GCTTGAAGTT ACTGCATTAT TTTATCAAGA	2880
AGTCTCTCT GCCTGTAAGT GTCCAAGGTT ATGACAGTAA ACAGTTTTA TTAAACATG	2940
AGTCACTATG GGATGAGAAA ATTGAAATAA AGCTACTGGG CCTCCTCTCA TAAAAGAGAC	3000
AGTTGTTGGC AAGGTAGCAA TACCAGTTc AAACttGGTG ACTTGATCCA CTATGCCTTA	3060
ATGGTTCCt CCATTGAGA AAATAAAGCT ATTCACATTG TTAAGAAAAA TACTTTAA	3120
AGTTTACCAT CAAGTCTTT TTATATTAT GTGTCTGTAT TCTACCCCTT TTTGCCTTAC	3180
AAGTGTATTT TGCAGGTTATT ATACCATTt TCTATTCTG GTGGCTTCTT CATAGCAGGT	3240

aagcctctcc ttctaaaaac ttctcaactg ttttcattha	aggaaaagaa aatgagtatt	3300
ttgtcctttt gtgtccctac agacacttc ttaaaccagt	tttggataa agaataactat	3360
ttccaaactc atattacaaa aacaaaataa aataataaaa	aaagaaaagca tgatattac	3420
tgtttgttg tctgggttg agaaaatgaaa tattgttcc	aattatttat aataaatcag	3480
tataaaaatgt tttatgattg ttatgtgtat tatgtaatac	gtacatgtt atggcaattt	3540
aacatgtgta ttctttcat ttaattgttt cagaatagga	taatttaggtt ttcgaatttt	3600
gtctttaaaa ttcatgtggt ttctatgcaa agttcttcat	atcatcacaa cattatttga	3660
ttaaataaaa attgaaaatg caccatggc agaaggagga	ggcagaatc atcacgaagt	3720
ggtgaagttc atggatgtct atcagcgcag ctactgccat	ccaatcgaga ccctggtgga	3780
catctccag gagtaccctg atgagatcga gtacatttc	aagccatcct gtgtccccct	3840
gatgcgatgc gggggctgct gcaatgacga gggctggag	tgtgtgcccct ctgaggagtc	3900
caacatcacc atgcagatta tgcggatcaa acctcacca	ggccagcaca taggagagat	3960
gagcttccta cagcacaaca aatgtgaatg cagaccaaag	aaagatagag caagacaaga	4020
aaaatgtgac aagccgagggc ggtga		4045

<210> 122

<211> 280

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 122

Met	Trp	Gln	Ile	Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala
1				5				10					15		

Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys
					20			25					30		

Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro
					35			40					45		

Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Pro	Tyr	Val	Ser	Asn	Ala
	50					55					60			

Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	Gln	Arg	Leu
65					70				75				80		

Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	Leu	Met	Lys
					85			90					95		

Val	Glu	Asn	Ile	Ser	Gln	Asp	Asn	Met	Lys	Glu	Met	Val	Glu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

100

105

110

Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
 115 120 125

Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
 130 135 140

Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
 145 150 155 160

Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
 165 170 175

Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
 180 185 190

Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
 195 200 205

Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
 210 215 220

Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala Thr Val Asn
 225 230 235 240

Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
 245 250 255

Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr
 260 265 270

Val Ala Lys Glu Glu Gln Ile Ser
 275 280

<210> 123

<211> 221

<212> PRT

<213> Homo sapiens

<400> 123

Glu Glu Glu Lys Pro Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly
 1 5 10 15

Phe Asn Lys Ser Gly Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu
 20 25 30

Pro Lys Lys Val Phe Cys Asn Met Asp Val Asn Gly Gly Trp Thr
 35 40 45

Val Ile Gln His Arg Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp
 50 55 60

Lys Glu Tyr Lys Met Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu
 65 70 75 80

Gly Asn Glu Phe Ile Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu
 85 90 95

Arg Ile Glu Leu Met Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr
 100 105 110

Asp Arg Phe His Ile Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu
 115 120 125

Lys Gly His Thr Gly Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His
 130 135 140

Gly Ala Asp Phe Ser Thr Lys Asp Ala Asp Asn Asp Asn Cys Met Cys
 145 150 155 160

Lys Cys Ala Leu Met Leu Thr Gly Gly Trp Trp Phe Asp Ala Cys Gly
 165 170 175

Pro Ser Asn Leu Asn Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly
 180 185 190

Lys Leu Asn Gly Ile Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser
 195 200 205

Leu Arg Ser Thr Thr Met Met Ile Arg Pro Leu Asp Phe
 210 215 220

<210> 124
 <211> 1506
 <212> DNA
 <213> Artificial sequence

<220>
 <221> misc_feature
 <222> ()...()
 <223> Synthetic

<400> 124
 atgtggcaga ttgtttctt tactctgagc tgtgatcttg tcttggccgc agcctataac 60
 aacttcgga agagcatgga cagcatagga aagaagcaat atcaggtcca gcatgggtcc 120
 tgcagctaca ct当地ctcctt gccagagatg gacaactgcc gcttccctc cagcccctac 180
 gtgtccaatg ctgtgcagag ggacgcgccc ctcgaatacg atgactcggt gcagaggctg 240
 caagtgcgtgg agaacatcat ggaaaacaac actcagtgcc taatgaaggt agagaatata 300
 tcccaggaca acatgaagaa agaaatggta gagatacagc agaatgcagt acagaaccag 360
 acggctgtga tgatagaaat agggacaaac ctgttgaacc aaacagcgga gcaaacgcgg 420
 aagttaactg atgtggaaagc ccaagtatta aatcagacca cgagacttga acttcagctc 480
 ttggaacact ccctctcgac aaacaaattt gaaaaacaga ttttggacca gaccagtgaa 540
 ataaacaaat tgcaagataa gaacagtttc ctagaaaaaga aggtgcttagc tatggaaagac 600
 aagcacatca tccaaactaca gtcaataaaa gaagagaaag atcagctaca ggtgttagta 660
 tccaaacgaga attccatcat tgaagaactc gaaaaaaaaa tagtgactgc cacggtaat 720

aattcagttc ttcagaagca gcaacatgat ctcatggaga cagttataa cttactgact 780
 atgatgtcca catcaaacgc agctaaggac cccactgttg ctaaagaaga acaaatcagc 840
 gaggaagaga aaccatttag agactgtgca gatgtatatc aagctggttt taataaaagt 900
 ggaatctaca ctattnatata taataatatg ccagaaccca aaaaggtgtt ttgcaatatg 960
 gatgtcaatg ggggaggttg gactgtataa caacatcgta aagatggaag tctagatttc 1020
 caaaggagct ggaaggaata taaaatgggt tttggaaatc cctccggta atattggctg 1080
 ggaaatgagt ttattnnnc cattaccagt cagaggcagt acatgctaag aattgagtt 1140
 atggactggg aagggAACCG agccttattca cagttatgaca gattccacat aggaaatgaa 1200
 aagcaaaact ataggttgta tttaaaaggt cacactggga cagcaggaaa acagagcagc 1260
 ctgatcttac acggtgctga ttccagcact aaagatgctg ataatgacaa ctgtatgtgc 1320
 aaatgtgccc tcattgttaac aggaggatgg tggtttcatg cttgtggccc ctccaaatcta 1380
 aatggaatgt tctataactgc gggacaaaac catggaaaac tgaatggat aaagtggcac 1440
 tacttcaaag ggcccagtta ctccttacgt tccacaacta tgatgattcg accttttagat 1500
 ttttga 1506

<210> 125

<211> 501

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 125

Met	Trp	Gln	Ile	Val	Phe	Phe	Thr	Leu	Ser	Cys	Asp	Leu	Val	Leu	Ala
1															

5

10

15

Ala	Ala	Tyr	Asn	Asn	Phe	Arg	Lys	Ser	Met	Asp	Ser	Ile	Gly	Lys	Lys

20

25

30

Gln	Tyr	Gln	Val	Gln	His	Gly	Ser	Cys	Ser	Tyr	Thr	Phe	Leu	Leu	Pro

35

40

45

Glu	Met	Asp	Asn	Cys	Arg	Ser	Ser	Ser	Pro	Tyr	Val	Ser	Asn	Ala

50

55

60

Val	Gln	Arg	Asp	Ala	Pro	Leu	Glu	Tyr	Asp	Asp	Ser	Val	Gln	Arg	Leu

65

70

75

80

Gln	Val	Leu	Glu	Asn	Ile	Met	Glu	Asn	Asn	Thr	Gln	Trp	Leu	Met	Lys

85

90

95

Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met Val Glu Ile
 100 105 110
 Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile Glu Ile Gly
 115 120 125
 Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys Leu Thr Asp
 130 135 140
 Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu Leu Gln Leu
 145 150 155 160
 Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln Ile Leu Asp
 165 170 175
 Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser Phe Leu Glu
 180 185 190
 Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln Leu Gln Ser
 195 200 205
 Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser Lys Gln Asn
 210 215 220
 Ser Ile Ile Glu Glu Leu Glu Lys Ile Val Thr Ala Thr Val Asn
 225 230 235 240
 Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu Thr Val Asn
 245 250 255
 Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys Asp Pro Thr
 260 265 270
 Val Ala Lys Glu Glu Gln Ile Ser Glu Glu Lys Pro Phe Arg Asp
 275 280 285
 Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly Ile Tyr Thr
 290 295 300
 Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Val Phe Cys Asn Met
 305 310 315 320
 Asp Val Asn Gly Gly Trp Thr Val Ile Gln His Arg Glu Asp Gly
 325 330 335
 Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met Gly Phe Gly
 340 345 350
 Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile Phe Ala Ile
 355 360 365
 Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met Asp Trp Glu
 370 375 380
 Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile Gly Asn Glu
 385 390 395 400
 Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly Thr Ala Gly
 405 410 415

Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser Thr Lys Asp
420 425 430

Ala Asp Asn Asp Asn Cys Met Cys Lys Cys Ala Leu Met Leu Thr Gly
435 440 445

Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn Gly Met Phe
450 455 460

Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile Lys Trp His
465 470 475 480

Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr Met Met Ile
485 490 495

Arg Pro Leu Asp Phe
500

<210> 126

<211> 648

<212> PRT

<213> Artificial sequence

<220>

<221> misc_feature

<222> ()..()

<223> Synthetic

<400> 126

Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
130 135 140

Pro Arg Arg Met Trp Gln Ile Val Phe Phe Thr Leu Ser Cys Asp Leu

145	150	155	160
Val Leu Ala Ala Ala Tyr Asn Asn Phe Arg Lys Ser Met Asp Ser Ile			
165		170	175
Gly Lys Lys Gln Tyr Gln Val Gln His Gly Ser Cys Ser Tyr Thr Phe			
180	185		190
Leu Leu Pro Glu Met Asp Asn Cys Arg Ser Ser Ser Pro Tyr Val			
195	200	205	
Ser Asn Ala Val Gln Arg Asp Ala Pro Leu Glu Tyr Asp Asp Ser Val			
210	215	220	
Gln Arg Leu Gln Val Leu Glu Asn Ile Met Glu Asn Asn Thr Gln Trp			
225	230	235	240
Leu Met Lys Val Glu Asn Ile Ser Gln Asp Asn Met Lys Lys Glu Met			
245		250	255
Val Glu Ile Gln Gln Asn Ala Val Gln Asn Gln Thr Ala Val Met Ile			
260	265	270	
Glu Ile Gly Thr Asn Leu Leu Asn Gln Thr Ala Glu Gln Thr Arg Lys			
275	280	285	
Leu Thr Asp Val Glu Ala Gln Val Leu Asn Gln Thr Thr Arg Leu Glu			
290	295	300	
Leu Gln Leu Leu Glu His Ser Leu Ser Thr Asn Lys Leu Glu Lys Gln			
305	310	315	320
Ile Leu Asp Gln Thr Ser Glu Ile Asn Lys Leu Gln Asp Lys Asn Ser			
325		330	335
Phe Leu Glu Lys Lys Val Leu Ala Met Glu Asp Lys His Ile Ile Gln			
340	345	350	
Leu Gln Ser Ile Lys Glu Glu Lys Asp Gln Leu Gln Val Leu Val Ser			
355	360	365	
Lys Gln Asn Ser Ile Ile Glu Glu Leu Glu Lys Lys Ile Val Thr Ala			
370	375	380	
Thr Val Asn Asn Ser Val Leu Gln Lys Gln Gln His Asp Leu Met Glu			
385	390	395	400
Thr Val Asn Asn Leu Leu Thr Met Met Ser Thr Ser Asn Ala Ala Lys			
405	410	415	
Asp Pro Thr Val Ala Lys Glu Glu Gln Ile Ser Glu Glu Lys Pro			
420	425	430	
Phe Arg Asp Cys Ala Asp Val Tyr Gln Ala Gly Phe Asn Lys Ser Gly			
435	440	445	
Ile Tyr Thr Ile Tyr Ile Asn Asn Met Pro Glu Pro Lys Lys Val Phe			
450	455	460	

Cys Asn Met Asp Val Asn Gly Gly Gly Trp Thr Val Ile Gln His Arg
465 470 475 480

Glu Asp Gly Ser Leu Asp Phe Gln Arg Gly Trp Lys Glu Tyr Lys Met
485 490 495

Gly Phe Gly Asn Pro Ser Gly Glu Tyr Trp Leu Gly Asn Glu Phe Ile
500 505 510

Phe Ala Ile Thr Ser Gln Arg Gln Tyr Met Leu Arg Ile Glu Leu Met
515 520 525

Asp Trp Glu Gly Asn Arg Ala Tyr Ser Gln Tyr Asp Arg Phe His Ile
530 535 540

Gly Asn Glu Lys Gln Asn Tyr Arg Leu Tyr Leu Lys Gly His Thr Gly
545 550 555 560

Thr Ala Gly Lys Gln Ser Ser Leu Ile Leu His Gly Ala Asp Phe Ser
565 570 575

Thr Lys Asp Ala Asp Asn Asn Cys Met Cys Lys Cys Ala Leu Met
580 585 590

Leu Thr Gly Trp Trp Phe Asp Ala Cys Gly Pro Ser Asn Leu Asn
595 600 605

Gly Met Phe Tyr Thr Ala Gly Gln Asn His Gly Lys Leu Asn Gly Ile
610 615 620

Lys Trp His Tyr Phe Lys Gly Pro Ser Tyr Ser Leu Arg Ser Thr Thr
625 630 635 640

Met Met Ile Arg Pro Leu Asp Phe
645